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<110> Anderson, John P.
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Elan Pharmaceuticals, Inc.

<120> BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS

<130> 015270-006430US

<140> US 09/471,669
<141> 1999-12-24

<150> US 60/114,408
<151> 1998-12-31

<150> US 60/119,571
<151> 1999-02-10

<150> US 60/139,172
<151> 1999-06-15

<160> 108

<170> PatentIn Ver. 2.1

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Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

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Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190

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225 230 235 240

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245 250 255

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260 265 270

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275 280 285

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325 330 335

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Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
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Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
450 455 460

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<213> Homo sapiens

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<210> 4
<211> 24

<212> DNA
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oligonucleotide primer derived from SEQ ID NO:2

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oligonucleotide primer derived from SEQ ID NO:2

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24

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<212> DNA
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oligonucleotide primer derived from SEQ ID NO:2

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24

<210> 7
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<212> DNA
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<211> 23
<212> DNA
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<210> 9
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oligonucleotide primer derived from SEQ ID NO:2

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<212> DNA
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oligonucleotide primer derived from SEQ ID NO:2

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<212> DNA
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23

<210> 12
<211> 23
<212> DNA
<213> Artificial Sequence

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oligonucleotide primer derived from SEQ ID NO:2

<400> 12
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23

<210> 13
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<212> DNA
<213> Artificial Sequence

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oligonucleotide primer derived from SEQ ID NO:2

<400> 13
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<210> 14
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Degenerate
oligonucleotide primer derived from SEQ ID NO:2

<400> 14
cgtcacagrt trtcgaccat ctc

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<210> 15
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide primer derived from SEQ ID NO:2

<400> 15
cgtcacagrt trtcaaccat ttc

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<210> 16
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<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide primer derived from SEQ ID NO:2

<400> 16
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<210> 17
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<212> DNA
<213> Artificial Sequence

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oligonucleotide primer derived from SEQ ID NO:2

<400> 17
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<210> 18
<211> 23
<212> DNA

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Degenerate
oligonucleotide primer derived from SEQ ID NO:2

<400> 18

cgtcacagrt trtcgaccat ttc

23

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

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<400> 19

gaggggcagc tttgtggaga

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<210> 20

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

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<400> 20

cagcataggc cagccccagg atgcct

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<210> 21

<211> 24

<212> DNA

<213> Artificial Sequence

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<400> 21

gtgatggcag caatgttggc acgc

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<210> 22

<211> 17

<212> DNA

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<221> misc_feature

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<223> n = a, c, g, or t.

<400> 22

gaygargagc cngagga

17

<210> 23

<211> 17

<212> DNA

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<221> misc_feature

<222> (1)..(17)

<223> n = a, c, g, or t.

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gaygargagc cngaaga

17

<210> 24

<211> 17

<212> DNA

<213> Artificial Sequence

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oligonucleotide primer

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<223> n = a, c, g, or t.

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gaygargaac cngagga

17

<210> 25

<211> 17

<212> DNA

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gaygargaac cngaaga

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<210> 32
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<400> 32
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<210> 33
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<212> DNA
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<400> 33
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<210> 34
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<210> 38
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oligonucleotide primer

<400> 38
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<210> 39
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<212> DNA
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<400> 39
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<210> 40
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<400> 40
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<210> 41
<211> 26
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oligonucleotide primer

<400> 41

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26

<210> 42
<211> 2348
<212> DNA
<213> Homo sapiens

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<210> 43
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<212> PRT
<213> Homo sapiens

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35 40 45

Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu
50 55 60

His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg
65 70 75 80

Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu
85 90 95

Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg
100 105 110

Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly
115 120 125

Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg
130 135 140

Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr
145 150 155 160

His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro
165 170 175

Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile
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Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro
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Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala
275 280 285

Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met
290 295 300

Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln
305 310 315 320

Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr
325 330 335

Lys Phe Ala, Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val
340 345 350

Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile
355 360 365

Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala
370 375 380

Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr
385 390 395 400

Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val
405 410 415

Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val
420 425 430

Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe
435 440 445

Ala Asp Asp Ile Ser Leu Leu Lys
450 455

<210> 44

<211> 2348

<212> DNA

<213> Homo sapiens

<400> 44

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<220>
<223> Description of Artificial Sequence: Flag sequence

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<211> 22
<212> PRT
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<400> 46
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<210> 47
<211> 23
<212> PRT
<213> Homo sapiens

<400> 47
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Leu Gly Leu Arg Leu Pro Arg
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Expression
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<220>

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<223> n = a, c, g, or t.

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gcgtcaacag cgtccgcag atcccgggca atgagatatg aaaaagcctg aactcaccgc 14580
gacgtctgtc gagaagttc tgatcgaaaa gttcgacagc gtctccgacc tgatgcagct 14640
ctcgaggggc gaagaatctc gtgcgttcag ctgcgtatgt a gggggcgtg gatatgtcct 14700
gccccgtaaat agctgcgcg atggtttcta caaagatcg tagtgggatc ggcactttgc 14760
atccggcccg ctcccccatt ccggaagtgc ttgacattgg ggaattcagc gagagcctga 14820
cctattgcat ctcccgccgt gcacagggtg tcacgttgca agacctgcct gaaaccgaac 14880
tgcccgctgt tctgcagccg gtgcggagg ccatggatgc gatcgctgcg gccgatctta 14940
gcccagcagc cgggttcggc ccattcgac cgcaaggaaat cggtaatac actacatggc 15000
gtgatttcat atgcgcgtt gctgatcccc atgtgtatca ctggcaaact gtgatggacg 15060
acaccgttag tgcgtccgtc ggcgcaggctc tcgatgagct gatgcttgg gccgaggact 15120
gccccgaagt ccggcacctc gtgcacgcgg atttcggctc caacaatgtc ctgacggaca 15180
atggccgcat aacagcggtc attgacttgg gcgaggcgat gttcgggat tcccaatacg 15240
agtcgccaa catcttcttc tggaggccgt ggttggcggt tatggagcag cagacgcgc 15300
acttcgagcg gaggcatccg gagcttgcag gatcgccgcg gctccggcg tatatgctcc 15360
gcattggctc tgaccaactc tatcagagct tgggttgcacgg caatttcgtat gatcagctt 15420
gggcgcaggc tcgatgcac gcaatcgcc gatccggagc cgggactgtc gggcgtacac 15480
aaatcgcccc cagaagcgcg gccgtcttgg ccgatggctg tgtagaagta ctcgcccata 15540
gtggaaacgg gagatgggg aggctaactg aaacacggaa ggagacaata cccgaaaggaa 15600
cccgcgctat gacggcaata aaaagacaga ataaaacgca cgggtgttgg gtcgtttgtt 15660
cataaaacgcg ggggttcggc ccagggtctgg cactctgtcg atacccacc gagaccccat 15720
tggggccaat acgcccgcgt ttcttcctt tccccacccc accccccaag ttccgggtgaa 15780
ggcccaggcc tcgcagccaa cgtcggggcg gcaggccctg ccataggccac tggcccccgt 15840
ggttagggac ggggtcccccc atggggatg gtttatggtt cgtgggggtt attatttgg 15900
gcgttgcgtg gggcttgcgtc cacgacttgg ctgagcagac agacccatgg ttttggatg 15960
gcctgggcat ggaccgcatt tactggcgccg acacgaacac cgggcgtctg tggctgccaa 16020
acaccccccga cccccaaaaa ccaccgcgcg gatttctggc gtgcgaagct agtcgaccaa 16080

<210> 49
<211> 32
<212> DNA
<213> Homo sapiens

<400> 49
cccgccgga gggcagctt tgtggagatg gt 32

<210> 50
<211> 11
<212> PRT
<213> Homo sapiens

<400> 50
Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
1 5 10

<210> 51
<211> 5
<212> PRT
<213> Homo sapiens

<400> 51
Val Asn Leu Asp Ala
1 5

<210> 52

<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligopeptide substrate

<400> 52
Ser Glu Val Asn Leu Asp Ala Glu Phe
1 5

<210> 53
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligopeptide substrate

<400> 53
Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile
1 5 10 15
Lys Thr Glu Glu Ile Ser Glu Val Asn Leu Asp Ala Glu Phe
20 25 30

<210> 54
<211> 5
<212> PRT
<213> Homo sapiens

<400> 54
Val Lys Met Asp Ala
1 5

<210> 55
<211> 24
<212> PRT
<213> Homo sapiens

<400> 55
Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
1 5 10 15
Glu Met Val Asp Asn Leu Arg Gly
20

<210> 56
<211> 15
<212> PRT
<213> Homo sapiens

<400> 56
Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg
1 5 10 15

<210> 57
<211> 419
<212> PRT
<213> Homo sapiens

<400> 57
Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15
Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30
Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45
Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60
Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80
Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95
Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110
Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125
Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140
Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160
Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175
Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190
Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
195 200 205
Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
210 215 220
Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225 230 235 240
Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
245 250 255
Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
260 265 270
Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
405 410 415

Val Ser Ala

<210> 58

<211> 407

<212> PRT

<213> Homo sapiens

<400> 58

Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
1 5 10 15

Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val
20 25 30

Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp
35 40 45

Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu
50 55 60

His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg
65 70 75 80

Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu
85 90 95

Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg
100 105 110

Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly
115 120 125

Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg
130 135 140

Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr
 145 150 155 160
 His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro
 165 170 175
 Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile
 180 185 190
 Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro
 195 200 205
 Ile Arg Arg Glu Trp Tyr Glu Val Ile Ile Val Arg Val Glu Ile
 210 215 220
 Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys
 225 230 235 240
 Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val
 245 250 255
 Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys
 260 265 270
 Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala
 275 280 285
 Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met
 290 295 300
 Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln
 305 310 315 320
 Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr
 325 330 335
 Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val
 340 345 350
 Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile
 355 360 365
 Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala
 370 375 380
 Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr
 385 390 395 400
 Asn Ile Pro Gln Thr Asp Glu
 405

<210> 59
 <211> 452
 <212> PRT
 <213> Homo sapiens

<400> 59
 Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
435 440 445

Gln Thr Asp Glu
450

<210> 60

<211> 420

<212> PRT

<213> Homo sapiens

<400> 60

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
1 5 10 15

Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 165 170 175
 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
 180 185 190
 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
 195 200 205
 Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
 210 215 220
 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
 225 230 235 240
 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
 245 250 255
 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
 260 265 270
 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
 275 280 285
 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
 290 295 300
 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
 305 310 315 320
 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
 325 330 335
 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
 340 345 350
 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
 355 360 365
 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
 370 375 380
 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
 385 390 395 400
 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
 405 410 415
 Val Ser Ala Cys
 420

<210> 61
 <211> 7
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 peptide inhibitor

<220>
<221> MOD_RES
<222> (4)
<223> Xaa = hydroxyethylene

<400> 61
Glu Val Met Xaa Ala Glu Phe
1 5

<210> 62
<211> 26
<212> PRT
<213> Homo sapiens

<400> 62
Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met
1 5 10 15
Leu Pro Leu Cys Leu Met Val Cys Gln Trp
20 25

<210> 63
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<223> P26-P4' sw peptide substrate

<400> 63
Cys Gly Gly Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu
1 5 10 15
Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Asn Leu Asp Ala Glu
20 25 30

Phe

<210> 64
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<223> P26-P1' peptide substrate with CGG linker

<400> 64
Cys Gly Gly Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu
1 5 10 15
Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Asn Leu
20 25

<210> 65
<211> 427
<212> PRT
<213> Mus sp.

<220>

<223> pBS/MuImPain H#3 construct

<400> 65

Ile Asp Lys Leu Asp Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met
1 5 10 15

Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met
20 25 30

Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly
35 40 45

Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg
50 55 60

Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly
65 70 75 80

Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr
85 90 95

Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn
100 105 110

Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn
115 120 125

Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp
130 135 140

Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile
145 150 155 160

Pro Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn
165 170 175

Gln Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly
180 185 190

Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg
195 200 205

Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly
210 215 220

Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile
225 230 235 240

Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu
245 250 255

Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro
260 265 270

Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr
275 280 285

Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu
290 295 300

Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu
305 310 315 320

Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe
325 330 335

Ala Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met
340 345 350

Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe
355 360 365

Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val
370 375 380

Glu Gly Pro Phe Val Thr Ala Asp Met Glu Asp Gly Tyr Asn Asn Arg
385 390 395 400

Ile Pro Ala Ala Arg Gly Ile His Phe Ser Gly Arg His Arg Gly Gly
405 410 415

Ala Pro Ile Arg Pro Ile Val Ser Arg Ile Asn
420 425

<210> 66
<211> 480
<212> PRT
<213> Homo sapiens

<400> 66

Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala
1 5 10 15

Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu
20 25 30

Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly
35 40 45

Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro
50 55 60

Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val
65 70 75 80

Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu
85 90 95

Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr
100 105 110

Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro
115 120 125

His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu
130 135 140

Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly
145 150 155 160

Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe
165 170 175

Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu
180 185 190

Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala
195 200 205

Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr
210 215 220

Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu
225 230 235 240

Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp
245 250 255

Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr
260 265 270

Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile
275 280 285

Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly
290 295 300

Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe
305 310 315 320

Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe
325 330 335

Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val
340 345 350

Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser
355 360 365

Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val
370 375 380

Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His
385 390 395 400

Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr
405 410 415

Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser
420 425 430

Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe
435 440 445

Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys
450 455 460

Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu Lys
465 470 475 480

<210> 67
<211> 444
<212> PRT
<213> Homo sapiens

<400> 67
Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln
1 5 10 15

Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn
20 25 30

Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro
35 40 45

His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr
50 55 60

Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp
65 70 75 80

Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn
85 90 95

Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe
100 105 110

Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala
115 120 125

Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu
130 135 140

Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly
145 150 155 160

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
165 170 175

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
180 185 190

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
195 200 205

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
210 215 220

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
225 230 235 240

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
245 250 255

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
260 265 270

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
275 280 285

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
290 295 300

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
305 310 315 320

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
325 330 335

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
340 345 350

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
355 360 365

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
370 375 380

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr
385 390 395 400

Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu
405 410 415

Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln
420 425 430

His Asp Asp Phe Ala Asp Asp Ile Ser Leu Leu Lys
435 440

<210> 68
<211> 395
<212> PRT
<213> Homo sapiens

<400> 68
Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln
1 5 10 15

Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn
20 25 30

Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro
35 40 45

His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr
50 55 60

Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp
65 70 75 80

Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn
85 90 95

Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe
100 105 110

Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala
115 120 125

Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu
130 135 140

Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly
145 150 155 160

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly
165 170 175

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu
180 185 190

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val
195 200 205

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr
210 215 220

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu
225 230 235 240

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser
245 250 255

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val
260 265 270

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser
275 280 285

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile
290 295 300

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln
305 310 315 320

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val
325 330 335

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala
340 345 350

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu
355 360 365

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu
370 375 380

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu
385 390 395

<210> 69
<211> 439
<212> PRT

<213> *Homo sapiens*

<400> 69

Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
1 5 10 15

Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr
20 25 30

Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His
35 40 45

Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys
50 55 60

Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly
65 70 75 80

Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala
85 90 95

Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser
100 105 110

Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro
115 120 125

Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His
130 135 140

Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu
145 150 155 160

Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly
165 170 175

Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile
180 185 190

Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn
195 200 205

Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser
210 215 220

Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe
225 230 235 240

Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe
245 250 255

Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly
260 265 270

Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly
275 280 285

Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr
290 295 300

Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys
305 310 315 320

Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile
325 330 335

Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
340 345 350

Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
355 360 365

Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
370 375 380

Ile Pro Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met
385 390 395 400

Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys
405 410 415

Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala
420 425 430

Asp Asp Ile Ser Leu Leu Lys
435

<210> 70
<211> 390
<212> PRT
<213> Homo sapiens

<400> 70
Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
1 5 10 15

Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr
20 25 30

Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His
35 40 45

Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys
50 55 60

Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly
65 70 75 80

Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala
85 90 95

Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser
100 105 110

Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro
115 120 125

Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His
130 135 140

Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu
145 150 155 160

Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly
165 170 175

Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile
180 185 190

Arg Arg Glu Trp Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn
195 200 205

Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser
210 215 220

Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe
225 230 235 240

Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe
245 250 255

Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly
260 265 270

Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly
275 280 285

Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr
290 295 300

Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys
305 310 315 320

Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile
325 330 335

Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
340 345 350

Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala
355 360 365

Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn
370 375 380

Ile Pro Gln Thr Asp Glu
385 390

<210> 71
<211> 374
<212> PRT
<213> Homo sapiens

<400> 71
Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
1 5 10 15

Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val
20 25 30

120

Glu* Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp
35 40 45

Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu
50 55 60

His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg
65 70 75 80

Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu
85 90 95

Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg
100 105 110

Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly
115 120 125

Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg
130 135 140

Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr
145 150 155 160

His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro
165 170 175

Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile
180 185 190

Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro
195 200 205

Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile
210 215 220

Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys
225 230 235 240

Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val
245 250 255

Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys
260 265 270

Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala
275 280 285

Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met
290 295 300

Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln
305 310 315 320

Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr
325 330 335

Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val
340 345 350

Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile
355 360 365

Gly Phe Ala Val Ser Ala
370

<210> 72
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: P10-P4'staD-V
peptide inhibitor

<220>
<221> MOD_RES
<222> (10)
<223> Xaa is statine moiety

<400> 72
Lys Thr Glu Glu Ile Ser Glu Val Asn Xaa Val Ala Glu Phe
1 5 10

<210> 73
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: P4-P4'staD-V
peptide inhibitor

<220>
<221> MOD_RES
<222> (5)
<223> Xaa is statine moiety

<400> 73
Ser Glu Val Asn Xaa Val Ala Glu Phe
1 5

<210> 74
<211> 431
<212> PRT
<213> Homo sapiens

<400> 74
Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala
1 5 10 15

Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu
20 25 30

Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly
35 40 45

Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro
50 55 60

Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val
65 70 75 80

Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu
85 90 95

Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr
100 105 110

Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro
115 120 125

His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu
130 135 140

Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly
145 150 155 160

Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe
165 170 175

Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu
180 185 190

Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala
195 200 205

Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr
210 215 220

Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu
225 230 235 240

Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp
245 250 255

Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr
260 265 270

Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile
275 280 285

Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly
290 295 300

Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe
305 310 315 320

Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe
325 330 335

Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val
340 345 350

Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser
355 360 365

Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val
370 375 380

Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His
385 390 395 400

Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr
405 410 415

Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu
420 425 430

<210> 75

<211> 361

<212> PRT

<213> Homo sapiens

<400> 75

Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu
1 5 10 15

Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr
20 25 30

Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His
35 40 45

Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys
50 55 60

Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly
65 70 75 80

Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala
85 90 95

Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser
100 105 110

Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro
115 120 125

Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His
130 135 140

Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu
145 150 155 160

Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly
165 170 175

Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile
180 185 190

Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn
195 200 205

Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser
210 215 220

Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe
225 230 235 240

Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe
245 250 255

Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly
260 265 270

Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly
275 280 285

Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr
290 295 300

Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys
305 310 315 320

Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile
325 330 335

Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly
340 345 350

Phe Ala Val Ser Ala Cys His Val His
355 360

<210> 76

<211> 63

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(63)

<223> n = a, c, g, or t.

<400> 76

garacngayg argarccnga rgarccnggn mgnmgnngnw snttygtnga ratggtngay 60
aay 63

<210> 77

<211> 21

<212> PRT

<213> Homo sapiens

<400> 77

Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
1 5 10 15

Glu Met Val Asp Asn

20

<210> 78

<211> 7

<212> PRT

<213> Artificial Sequence

<220> .
<223> Description of Artificial Sequence: Peptide
inhibitor P3-P4' XD-V

<220>
<221> MOD_RES
<222> (3)
<223> Xaa is hydroxyethylene or statine

<400> 78
Val Met Xaa Val Ala Glu Phe
1 5

<210> 79
<211> 11
<212> PRT
<213> Homo sapiens

<400> 79
Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val
1 5 10

<210> 80
<211> 419
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nucleotide
insert in vector pCF

<400> 80
ctgtgggct cgcgggttag gacaaactct tcgcggctt tccagttactc ttggatcgaa 60
aaccgtcggt cctccgaacg gtactccgccc accgaggggac ctgagcgagt cccatcgac 120
cgatcgaa aacctctcgaa ctgtgggtt gagttactccc tctcaaaagc gggcatgact 180
tctgcgttaa gattgtcagt ttccaaaaac gaggaggatt tgatattcac ctggcccg 240
gtatgcctt tgagggtggc cgcgtccatc tggcagaaaa agacaatctt ttgttgtaa 300
agcttgagggt gtggcaggct tgagatctgg ccatacactt gagtgacaaat gacatccact 360
ttgcctttctt ctccacaggt gtccactccc aggtccaact gcaggtcgac tctagaccc 419

<210> 81
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide
inhibitor P4-P4' XD-V

<220>
<221> MOD_RES
<222> (4)
<223> Xaa is hydroxyethylene or statine.

<400> 81
Glu Val Met Xaa Val Ala Glu Phe
1 5

<210> 82
<211> 9
<212> PRT
<213> Homo sapiens

<400> 82
Ser Glu Val Lys Met Asp Ala Glu Phe
1 5

<210> 83
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> APP fragment P5-P4' wt

<400> 83
Ser Glu Val Asn Leu Asp Ala Glu Phe
1 5

<210> 84
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: APP fragment

<400> 84
Ser Glu Val Lys Leu Asp Ala Glu Phe
1 5

<210> 85
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: APP fragment

<400> 85
Ser Glu Val Lys Phe Asp Ala Glu Phe
1 5

<210> 86
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: APP fragment

<400> 86
Ser Glu Val Asn Phe Asp Ala Glu Phe
1 5

<210> 87
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: APP fragment

<400> 87
Ser Glu Val Lys Met Ala Ala Glu Phe
1 5

<210> 88
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: APP fragment

<400> 88
Ser Glu Val Asn Leu Ala Ala Glu Phe
1 5

<210> 89
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: APP fragment

<400> 89
Ser Glu Val Lys Leu Ala Ala Glu Phe
1 5

<210> 90
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: APP fragment

<400> 90
Ser Glu Val Lys Met Leu Ala Glu Phe
1 5

<210> 91
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: APP fragment

<400> 91
Ser Glu Val Asn Leu Leu Ala Glu Phe
1 5

<210> 92
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: APP fragment

<400> 92
Ser Glu Val Lys Leu Leu Ala Glu Phe
1 5

<210> 93
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: APP fragment

<400> 93
Ser Glu Val Lys Phe Ala Ala Glu Phe
1 5

<210> 94
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: APP fragment

<400> 94
Ser Glu Val Asn Phe Ala Ala Glu Phe
1 5

<210> 95
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: APP fragment

<400> 95
Ser Glu Val Lys Phe Leu Ala Glu Phe
1 5

<210> 96
<211> 9
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: APP fragment

<400> 96

Ser Glu Val Asn Phe Leu Ala Glu Phe
1 5

<210> 97

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: APP-derived
fragment P10-P4' (D-V)

<400> 97

Lys Thr Glu Glu Ile Ser Glu Val Asn Leu Val Ala Glu Phe
1 5 10

<210> 98

<211> 35

<212> DNA

<213> Homo sapiens

<400> 98

cccgaaagagc ccggccggag gggcagctt gtcga

35

<210> 99

<211> 11

<212> PRT

<213> Homo sapiens

<400> 99

Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg
1 5 10

<210> 100

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: N terminal
peptide of beta-secretase secreted from 293T cells

<400> 100

Thr Gln His Gly Ile Arg Leu Pro Leu Arg
1 5 10

<210> 101

<211> 9

<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: N-terminal
peptide sequence of beta-secretase secreted from
293T cells

<400> 101
Met Val Asp Asn Leu Arg Gly Lys Ser
1 5

<210> 102
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: N terminal
peptide sequence of a form of beta-secretase
isolated from recombinant CosA2 cells.

<400> 102
Gly Ser Phe Val Glu Met Val Asp Asn Leu
1 5 10

<210> 103
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Beta-secretase
cleavage site in wild-type APP sequence

<400> 103
Val Lys Met Asp
1

<210> 104
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Beta-secretase
cleavage site in APP bearing Swedish mutation

<400> 104
Val Asn Leu Asp
1

<210> 105
<211> 408
<212> PRT
<213> Mus sp.

<220>
<223> pBS/MuImPain E17 #11 construct

<400> 105

Ser Ile Ser Leu Ile Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met
1 5 10 15

Val Asn Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met
20 25 30

Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly
35 40 45

Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg
50 55 60

Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly
65 70 75 80

Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr
85 90 95

Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn
100 105 110

Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn
115 120 125

Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp
130 135 140

Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile
145 150 155 160

Pro Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn
165 170 175

Gln Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly
180 185 190

Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg
195 200 205

Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly
210 215 220

Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile
225 230 235 240

Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu
245 250 255

Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro
260 265 270

Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr
275 280 285

Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu
290 295 300

Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu
305 310 315 320

132

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Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe
325 330 335

Ala Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met
340 345 350

Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe
355 360 365

Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val
370 375 380

Glu Gly Pro Phe Val Thr Ala Asp Met Glu Asp Cys Gly Tyr Asn Asn
385 390 395 400

Arg Ile Pro Ala Ala Arg Gly Ile
405

<210> 106

<211> 401

<212> PRT

<213> Mus sp.

<220>

<223> pBS/MuImPain E17 #14 construct

<400> 106

Lys Leu Asp Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp
1 5 10 15

Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val
20 25 30

Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser
35 40 45

Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr
50 55 60

Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr
65 70 75 80

Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu
85 90 95

Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala
100 105 110

Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu
115 120 125

Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser
130 135 140

Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile Pro Asn
145 150 155 160

Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Thr
165 170 175

Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp
180 185 190

His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu
195 200 205

Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp
210 215 220

Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp
225 230 235 240

Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala
245 250 255

Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly
260 265 270

Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro
275 280 285

Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr
290 295 300

Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro
305 310 315 320

Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Val
325 330 335

Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly
340 345 350

Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val
355 360 365

Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly
370 375 380

Pro Phe Val Thr Ala Asp Met Glu Asp Cys Gly Tyr Asn Asn Arg Ile
385 390 395 400

Gln

<210> 107
<211> 231
<212> PRT
<213> Mus sp.

<220>
<223> pBS/MuImPain E17 Brain #17 construct

<400> 107
Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr
1 5 10 15

Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu
20 25 30

Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro
 35 40 45
 Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp
 50 55 60
 Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly
 65 70 75 80
 Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr
 85 90 95
 Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Val
 100 105 110
 Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile
 115 120 125
 Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys
 130 135 140
 Gln Thr His Ile Pro Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly
 145 150 155 160
 Phe Pro Leu Asn Gln Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met
 165 170 175
 Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr
 180 185 190
 Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val
 195 200 205
 Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr
 210 215 220
 Asp Lys Ser Ile Val Asp Ser
 225 230

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 <213> Mus sp.

<220>
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<400> 108
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 1 5 10 15

Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu
 20 25 30

Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro
 35 40 45

Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp
 50 55 60

Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly
65 70 75 80

Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr
85 90 95

Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile
100 105 110

Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile
115 120 125

Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys
130 135 140

Gln Thr His Ile Pro Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly
145 150 155 160

Phe Pro Leu Asn Gln Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met
165 170 175

Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr
180 185 190

Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val
195 200 205

Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr
210 215 220

Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys
225 230 235 240

Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr
245 250 255

Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp
260 265 270

Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr
275 280 285

Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro
290 295 300

Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp
305 310 315 320

Cys Tyr Lys Phe Ala Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly
325 330 335

Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys
340 345 350

Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg
355 360 365

Thr Ala Ala Val Glu Gly Pro Phe Val Thr Ala Asp
370 375 380